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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT:
 - (A) NAME: LeukoSite, Inc.
 - (B) STREET: 215 First Street

 - (C) CITY: Cambridge
 (D) STATE/PROVINCE: Massachusetts
 - (E) COUNTRY: U.S.A.
 - (F) POSTAL CODE/ZIP: 02142
 - (G) TELEPHONE: (617) 621-9350 (I) TELEFAX: (617) 621-9349
- (i) APPLICANT/INVENTOR:
 - (A) NAME: Michael J. Briskin
 - (B) STREET: 28 Harbell Street
 - (C) CITY: Lexington
 - (D) STATE/PROVINCE: Massachusetts

 - (E) COUNTRY: U.S.A.
 (F) POSTAL CODE/ZIP: 02173
- (i) APPLICANT/INVENTOR:

 - (A) NAME: Douglas J. Ringler
 (B) STREET: 382 Ocean Avenue, #1008
 - (C) CITY: Revere
 - (D) STATE/PROVINCE: Massachusetts
 - (E) COUNTRY: U.S.A.
 - (F) POSTAL CODE/ZIP: 02151
- (i) APPLICANT/INVENTOR:
 - (A) NAME: Dominic Picarella
 - (B) STREET: 2 North Bennet Court, #4
 - (C) CITY: Boston
 - (D) STATE/PROVINCE: Massachusetts

 - (E) COUNTRY: U.S.A.
 (F) POSTAL CODE/ZIP: 02113
- (i) APPLICANT/INVENTOR:
 - (A) NAME: Walter Newman
 - (B) STREET: 3 Durham Street, #3
 - (C) CITY: Boston
 - (D) STATE/PROVINCE: Massachusetts
 - (E) COUNTRY: U.S.A.
 - (F) POSTAL CODE/ZIP: 02115
- (ii) TITLE OF INVENTION: Mucosal Vascular Addressins and Uses Thereof
- (iii) NUMBER OF SEQUENCES: 13
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 - (B) STREET: Two Militia Drive
 - (C) CITY: Lexington
 - (D) STATE: Massachusetts
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 02173~4799

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- (A) MEDIUM TYPE: Floppy disk

- (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/523,004
- (B) FILING DATE: 01-SEP-1995

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/386,857
- (B) FILING DATE: 10-FEB-1995

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Brook, David E.
- (B) REGISTRATION NUMBER: 22,592
- (C) REFERENCE/DOCKET NUMBER: LKS94-04A2 PCT

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 617-861-6240 (B) TELEFAX: 617-861-9540

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1624 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1218

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| Met | GAT Asp | Phe | Gly | Leu | Ala | | | | | | | | | | CTC Leu | 48 |
|-----|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------------|----|
| CTC | GGC | CAG | TCC | CTC | CAG | GTG | AAG | ccc | CTG | CAG | GTG | GAG | ccc | CCG | GAG | 96 |

Leu Gly Gln Ser Leu Gln Val Lys Pro Leu Gln Val Glu Pro Pro Glu

CCG GTG GCC GTG GCC TTG GGC GCC TCG CGC CAG CTC ACC TGC CGC 144 Pro Val Val Ala Val Ala Leu Gly Ala Ser Arg Gln Leu Thr Cys Arg



| CT(Le | G GC | а Су | s Al | G GA | C CG | C GGC G Gly 55 | Ala | TC Se: | G GTO | G CAG | G TG | p Ar | G GG g Gl | C CT y Le | G GAC | 192 |
|-------------------|-------------------|-------------------|-----------------------|----------------------|-------------------|----------------------|-------------------|-------------------|-------------------|----------------------|-------------------|-------------------|---------------------|----------------------|----------------------|-----|
| ACC Thi | : Se | C CT | G GGG | C GCG Y Ala | G GT0 a Val | l Glr | TCC Ser | G GA | C ACC | G GGG G Gly 75 | Ar | C AG g Se | C GTO | C CT | C ACC u Thr 80 | 240 |
| GT(Va] | G CG(| AA AB | C GCC n Ala | C TCC a Ser 85 | Let | TCG Ser | GCG | GC0 Ala | GGG Gly 90 | Thi | C CGC | C GTO | G TGO | C GT6 5 Va. 9: | G GGC l Gly | 288 |
| TCC Ser | TGC Cys | C GGG G Gly | G GGG Y Gly 100 | Arc | ACC Thr | TTC Phe | CAG Gln | CAC Hie 105 | Thr | GTC Val | CAC Glr | CTO | C CTI Let 110 | ı Val | G TAC L Tyr | 336 |
| GCC Ala | TTC Phe | Pro | Asp | CAG Glr | CTG Leu | ACC Thr | GTC Val 120 | Ser | CCA Pro | GCA Ala | GCC Ala | CTC Let 125 | ı Val | CC1 | GGT Gly | 384 |
| GAC Asp | Pro 130 | Glu | GTG Val | GCC Ala | TGT Cys | ACG Thr 135 | GCC Ala | CAC | AAA Lys | GTC Val | ACG Thr 140 | Pro | GTG Val | GAC Asp | CCC Pro | 432 |
| AAC Asn 145 | Ala | CTC Leu | C TCC Ser | TTC Phe | TCC Ser 150 | CTG Leu | CTC Leu | GTC Val | GGG Gly | GGC Gly 155 | CAG Gln | GAA Glu | CTG Leu | GAG Glu | GGG Gly 160 | 480 |
| GCG Ala | CAA Gln | GCC | CTG Leu | GGC Gly 165 | CCG Pro | GAG Glu | GTG Val | CAG Gln | GAG Glu 170 | GAG Glu | GAG Glu | GAG Glu | GAG Glu | CCC Pro 175 | CAG Gln | 528 |
| GGG Gly | GAC Asp | GAG Glu | GAC Asp 180 | GTG Val | CTG Leu | TTC Phe | AGG Arg | GTG Val 185 | ACA Thr | GAG Glu | CGC Arg | TGG Trp | CGG Arg 190 | CTG Leu | CCG Pro | 576 |
| CCC Pro | CTG Leu | GGG Gly 195 | ACC Thr | CCT Pro | GTC Val | CCG Pro | CCC Pro 200 | GCC Ala | CTC Leu | TAC Tyr | TGC Cys | CAG Gln 205 | GCC Ala | ACG Thr | ATG Met | 624 |
| AGG Arg | CTG Leu 210 | CCT Pro | GGC Gly | TTG Leu | GAG Glu | CTC Leu 215 | AGC Ser | CAC His | CGC Arg | CAG Gln | GCC Ala 220 | ATC Ile | CCC Pro | GTC Val | CTG Leu | 672 |
| CAC His 225 | AGC Ser | CCG Pro | ACC Thr | TCC Ser | CCG Pro 230 | GAG Glu | CCT Pro | CCC Pro | GAC Asp | ACC Thr 235 | ACC Thr | TCC Ser | CCG Pro | GAG Glu | CCT Pro 240 | 720 |
| CCC Pro | AAC Asn | ACC Thr | ACC Thr | TCC Ser 245 | CCG Pro | GAG Glu | TCT Ser | CCC Pro | GAC Asp 250 | ACC Thr | ACC Thr | TCC Ser | CCG Pro | GAG Glu 255 | TCT Ser | 768 |
| CCC Pro | GAC Asp | ACC Thr | ACC Thr 260 | TCC Ser | CAG Gln | GAG Glu | Pro | CCC Pro 265 | GAC Asp | ACC Thr | ACC Thr | TCC Ser | CAG Gln 270 | GAG Glu | CCT Pro | 816 |
| CCC Pro | Asp | ACC Thr 275 | ACC Thr | TCC Ser | CAG Gln | Glu : | CCT Pro 280 | CCC Pro | GAC . Asp | ACC Thr | Thr | TCC Ser 285 | CCG Pro | GAG Glu | CCT Pro | 864 |

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| CCC Pro | GAC Asp 290 | AAG Lys | ACC Thr | TCC Ser | CCG Pro | GAG Glu 295 | CCC Pro | GCC Ala | CCC Pro | CAG Gln | CAG Gln 300 | GGC Gly | TCC Ser | ACA Thr | CAC His | 912 |
|-------------------|-------------------|-------------------|-------------------|---------------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| ACC Thr 305 | CCC Pro | AGG Arg | AGC Ser | CCA Pro | GGC Gly 310 | TCC Ser | ACC Thr | AGG Arg | ACT Thr | CGC Arg 315 | CGC Arg | CCT Pro | GAG Glu | ATC Ile | TCC Ser 320 | 960 |
| CAG Gln | GCT Ala | GGG Gly | CCC Pro | ACG Thr 325 | CAG Gln | GGA Gly | GAA Glu | GTG Val | ATC Ile 330 | CCA Pro | ACA Thr | GGC Gly | TCG Ser | TCC Ser 335 | AAA Lys | 1008 |
| CCT Pro | GCG Ala | GGT Gly | GAC Asp 340 | CAG Gln | CTG Leu | CCC Pro | GCG Ala | GCT Ala 345 | CTG Leu | TGG Trp | ACC Thr | AGC Ser | AGT Ser 350 | GCG Ala | GTG Val | 1056 |
| CTG Leu | GGA Gly | CTG Leu 355 | CTG Leu | CTC Leu | CTG Leu | GCC Ala | TTG Leu 360 | CCC Pro | ACG Thr | TAT Tyr | CAC His | CTC Leu 365 | TGG Trp | AAA Lys | CGC Arg | 1104 |
| TGC Cys | CGG Arg 370 | CAC His | CTG Leu | GCT Ala | GAG Glu | GAC Asp 375 | GAC Asp | ACC Thr | CAC His | CCA Pro | CCA Pro 380 | GCT Ala | TCT Ser | CTG Leu | AGG Arg | 1152 |
| CTT Leu 385 | CTG Leu | CCC Pro | CAG Gln | GTG Val | TCG Ser 390 | GCC Ala | TGG Trp | GCT Ala | GGG Gly | TTA Leu 395 | AGG Arg | GGG Gly | ACC Thr | Gly | CAG Gln 400 | 1200 |
| GTC Val | GGG Gly | ATC Ile | Ser | CCC Pro 4 05 | TCC Ser | TGAG | TGGC | CA G | CCTT | TCCC | C CT | GTGA | AAGC | | | 1248 |
| AAAA | TAGC | TT G | GACC | CCTT | C AA | GTTG. | AGAA | CTG | GTCA | GGG | CAAA | CCTG | сс т | CCCA | TTCTA | 1308 |
| CTCA | AAGT | CA T | CCCT | CTGC | T CA | CAGA | GATG | GAT | GCAT | GTT | CTGA | TTGC | CT C | TTTG | GAGAA | 1368 |
| GCTC | ATCA | GA A | ACTC. | AAAA | G AA | GGCC | ACTG | TTT | GTCT | CAC | CTAC | CCAT | GA C | CTGA | AGCCC | 1428 |
| CTCC | CTGA | GT G | GTCC | CCAC | C TT | TCTG | GACG | GAA | CCAC | GTA (| CTTT | TTAC | AT A | CATTO | GATTC | 1488 |
| ATGT | CTCA | CG T | CTCC | CTAA | A AA | TGCG | FAAG | ACC | AAGC: | TGT (| gada: | TGAC | CA C | CCTG | GCCC | 1548 |
| CTGT | CGTC | AG G | ACCT | CCTG | A GG | CTTTC | GGCA | AAT | AAAC | CTC (| CTAA | AATG | LA TA | AAAA | AAAA | 1608 |
| AAAA | AAAA | AA AA | AAAA | A | | | | | | | | | | | | 1624 |

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 406 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asp Phe Gly Leu Ala Leu Leu Leu Ala Gly Leu Leu Gly Leu Leu 10



Leu Gly Gln Ser Leu Gln Val Lys Pro Leu Gln Val Glu Pro Pro Glu Pro Val Val Ala Val Ala Leu Gly Ala Ser Arg Gln Leu Thr Cys Arg Leu Ala Cys Ala Asp Arg Gly Ala Ser Val Gln Trp Arg Gly Leu Asp Thr Ser Leu Gly Ala Val Gln Ser Asp Thr Gly Arg Ser Val Leu Thr Val Arg Asn Ala Ser Leu Ser Ala Ala Gly Thr Arg Val Cys Val Gly 85 90 95 Ser Cys Gly Gly Arg Thr Phe Gln His Thr Val Gln Leu Leu Val Tyr 105 Ala Phe Pro Asp Gln Leu Thr Val Ser Pro Ala Ala Leu Val Pro Gly Asp Pro Glu Val Ala Cys Thr Ala His Lys Val Thr Pro Val Asp Pro Asn Ala Leu Ser Phe Ser Leu Leu Val Gly Gly Gln Glu Leu Glu Gly Ala Gln Ala Leu Gly Pro Glu Val Gln Glu Glu Glu Glu Pro Gln Gly Asp Glu Asp Val Leu Phe Arg Val Thr Glu Arg Trp Arg Leu Pro Pro Leu Gly Thr Pro Val Pro Pro Ala Leu Tyr Cys Gln Ala Thr Met Arg Leu Pro Gly Leu Glu Leu Ser His Arg Gln Ala Ile Pro Val Leu His Ser Pro Thr Ser Pro Glu Pro Pro Asp Thr Thr Ser Pro Glu Pro Pro Asn Thr Thr Ser Pro Glu Ser Pro Asp Thr Thr Ser Pro Glu Ser 250 Pro Asp Thr Thr Ser Gln Glu Pro Pro Asp Thr Thr Ser Gln Glu Pro 265 Pro Asp Thr Thr Ser Gln Glu Pro Pro Asp Thr Thr Ser Pro Glu Pro Pro Asp Lys Thr Ser Pro Glu Pro Ala Pro Gln Gln Gly Ser Thr His 300 Thr Pro Arg Ser Pro Gly Ser Thr Arg Thr Arg Arg Pro Glu Ile Ser Gln Ala Gly Pro Thr Gln Gly Glu Val Ile Pro Thr Gly Ser Ser Lys Pro Ala Gly Asp Gln Leu Pro Ala Ala Leu Trp Thr Ser Ser Ala Val

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Leu Gly Leu Leu Leu Ala Leu Pro Thr Tyr His Leu Trp Lys Arg 360

Cys Arg His Leu Ala Glu Asp Asp Thr His Pro Pro Ala Ser Leu Arg 370 375

Leu Leu Pro Gln Val Ser Ala Trp Ala Gly Leu Arg Gly Thr Gly Gln 385

Val Gly Ile Ser Pro Ser

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1539 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..1146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| ATG Met 1 | GAT Asp | TTC Phe | GGA Gly | CTG Leu 5 | GCC Ala | CTC Leu | CTG Leu | CTG Leu | GCG Ala 10 | GGG Gly | CTT Leu | CTG Leu | GGG Gly | CTC Leu 15 | CTC Leu | 48 |
|------------------|------------------|------------------|-------------------|------------------|------------------|------------------|------------------|-------------------|------------------|------------------|------------------|------------------|-------------------|------------------|------------------|-----|
| CTC Leu | GGC Gly | CAG Gln | TCC Ser 20 | CTC Leu | CAG Gln | GTG Val | AAG Lys | CCC Pro 25 | CTG Leu | CAG Gln | GTG Val | GAG Glu | CCC Pro 30 | CCG Pro | GAG Glu | 96 |
| CCG Pro | GTG Val | GTG Val 35 | GCC Ala | GTG Val | GCC Ala | TTG Leu | GGC Gly 40 | GCC Ala | TCG Ser | CGC Arg | CAG Gln | CTC Leu 45 | ACC Thr | TGC Cys | CGC Arg | 144 |
| CTG Leu | GCC Ala 50 | TGC Cys | GCG Ala | GAC Asp | CGC Arg | GGG Gly 55 | GCC Ala | TCG Ser | GTG Val | CAG Gln | TGG Trp 60 | CGG Arg | GGC Gly | CTG Leu | GAC Asp | 192 |
| ACC Thr 65 | AGC Ser | CTG Leu | GGC Gly | GCG Ala | GTG Val 70 | CAG Gln | TCG Ser | GAC Asp | ACG Thr | GGC Gly 75 | CGC Arg | AGC Ser | GTC Val | CTC Leu | ACC Thr 80 | 240 |
| GTG Val | CGC Arg | AAC Asn | GCC Ala | TCG Ser 85 | CTG Leu | TCG Ser | GCG Ala | GCC Ala | GGG Gly 90 | ACC Thr | CGC Arg | GTG Val | TGC Cys | GTG Val 95 | GGC Gly | 288 |
| TCC Ser | TGC Cys | GGG Gly | GGC Gly 100 | CGC Arg | ACC Thr | TTC Phe | CAG Gln | CAC His 105 | ACC Thr | GTG Val | CAG Gln | CTC Leu | CTT Leu 110 | GTG Val | TAC Tyr | 336 |



| GC Al | C TT a Ph | C CC e Pr 11 | o Asj | C CA | G CT n Le | G AC | C GT r Va 12 | C TC l Se O | C CC r Pr | A GC O Al | A GC a Al | CC CT | eu Va | rg c | CT ro | GGT Gly | 384 |
|-------------------|---------------------|--------------------|-------------------|-------------------|---------------------|-----------------------|--------------------|-------------------|-----------------------|--------------------|--------------------|-----------------------|--------------------|-------------------|----------------|-------------------|------|
| GA(As) | C CC P Pro 13 | O GT | G GTO u Val | G GC0 | C TG | T ACC 5 Thi 135 | r Al | C CAG | C AA B Ly | A GT s Va | C AC l Th 14 | r Pr | CC G1 | TG G | ac sp | ccc Pro | 432 |
| AA(As: 145 | JAL | G CTO | C TCC | TTO Phe | C TCC Ser 150 | r Lei | CTO | C GTO | C GGG | G GG y Gl 15 | y Gl | G GA n Gl | A CI u Le | 'G G | AG lu | GGG Gly 160 | 480 |
| GCC Ala | G CAM | A GCG | C CTC | GGG Gly 165 | Pro | G GAC | GTC Val | G CAC | G GAG 1 Glu 170 | ı Gl | G GA | G GA u Gl | G GA u Gl | u Pi | CC CO 75 | CAG Gln | 528 |
| GGG Gly | GAC Asp | GAC Glu | GAC Asp 180 |) Val | Leu | TTC Phe | AGC Arç | GTC Val 185 | . Thi | A GAO | G CG | C TG g Tr | G CG p Ar 19 | g Le | rG ≥u | CCG Pro | 576 |
| CCC Pro | CTC Leu | GGG Gly 195 | Thr | Pro | GTC Val | ccc Pro | Pro 200 | GCC Ala | CTC Leu | TAC Tyr | TG0 | C CAC 5 Gl: 20: | n Al | C Ac | G . | ATG Met | 624 |
| Arg | 210 | Pro | Gly | Leu | Glu | Leu 215 | Ser | CAC His | Arg | Glr | 220 | a Ile | e Pro | o Va | 1 1 | Leu | 672 |
| 225 | ser | Pro | Inr | ser | 230 | Glu | Pro | ccc Pro | Asp | Thr 235 | Thr | Ser | Pro | G1 | u 5 | Ser 240 | 720 |
| PIO | Asp | inr | Thr | 245 | Pro | Glu | Ser | CCC Pro | 250 | Thr | Thr | Ser | Glr | G1 25 | u F 5 | Pro | 768 |
| CCC Pro | GAC Asp | ACC Thr | ACC Thr 260 | TCC Ser | CCG Pro | GAG Glu | CCT Pro | CCC Pro 265 | GAC Asp | AAG Lys | ACC Thr | TCC | Pro 270 | Gl | G C | ccc ecc | 816 |
| GCC Ala | CCC Pro | CAG Gln 275 | CAG Gln | GGC Gly | TCC Ser | ACA Thr | CAC His 280 | ACC Thr | CCC Pro | AGG Arg | AGC Ser | CCA Pro 285 | GGC Gly | TC(Se) | C A | CC hr | 864 |
| AGG Arg | ACT Thr 290 | CGC Arg | CGC Arg | CCT Pro | GAG Glu | ATC Ile 295 | TCC Ser | CAG Gln | GCT Ala | GGG Gly | CCC Pro 300 | ACG Thr | CAG Gln | GG# Gly | A G | AA lu | 912 |
| GTG Val 305 | ATC Ile | CCA Pro | ACA Thr | GGC Gly | TCG Ser 310 | TCC Ser | AAA Lys | CCT Pro | GCG Ala | GGT Gly 315 | GAC Asp | CAG Gln | CTG Leu | CCC | A | CG la 20 | 960 |
| GCT Ala | CTG Leu | TGG Trp | Thr | AGC Ser 325 | AGT Ser | GCG Ala | GTG Val | CTG Leu | GGA Gly 330 | CTG Leu | CTG Leu | CTC Leu | CTG Leu | GCC Ala 335 | Le | TG eu | 1008 |
| CCC Pro | ACC Thr | Tyr | CAC His 340 | CTC Leu | TGG Trp | AAA Lys . | CGC Arg | TGC Cys 345 | CGG Arg | CAC His | CTG Leu | GCT Ala | GAG Glu 350 | GAC Asp | GA As | AC Sp | 1056 |

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| ACC CAC CCA CCA GC Thr His Pro Pro Al 355 | TCT CTG AGG a Ser Leu Arg 360 | CTT CTG CCC Leu Leu Pro | CAG GTG TCG GCC TGG Gln Val Ser Ala Trp 365 | 1104 |
|---|-------------------------------------|----------------------------|---|------|
| GCT GGG TTA AGG GG Ala Gly Leu Arg Gl 370 | G ACC GGC CAG Thr Gly Gln 375 | GTC GGG ATC Val Gly Ile | AGC CCC TCC Ser Pro Ser 380 | 1146 |
| TGAGTGGCCA GCCTTTC | CC CTGTGAAAG | AAAATAGCTT | GGACCCCTTC AAGTTGAGAA | 1206 |
| CTGGTCAGGG CAAACCT | CC TCCCATTCT | CTCAAAGTCA | TCCCTCTGTT CACAGAGATG | 1266 |
| GATGCATGTT CTGATTG | CT CTTTGGAGA | GCTCATCAGA | AACTCAAAAG AAGGCCACTG | 1326 |
| TTTGTCTCAC CTACCCA | GA CCTGAAGCCC | CTCCCTGAGT | GGTCCCCACC TTTCTGGACG | 1386 |
| GAACCACGTA CTTTTTAC | AT ACATTGATTO | ATGTCTCACG | TCTCCCTAAA AATGCGTAAG | 1446 |
| ACCAAGCTGT GCCCTGAC | CA CCCTGGGCCC | CTGTCGTCAG | GACCTCCTGA GGCTTTGGCA | 1506 |
| AATAAACCTC CTAAAATG | AAAAAAAA AA | AAA | | 1539 |

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 382 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asp Phe Gly Leu Ala Leu Leu Leu Ala Gly Leu Leu Gly Leu Leu

Leu Gly Gln Ser Leu Gln Val Lys Pro Leu Gln Val Glu Pro Pro Glu

Pro Val Val Ala Val Ala Leu Gly Ala Ser Arg Gln Leu Thr Cys Arg 35 40 45

Leu Ala Cys Ala Asp Arg Gly Ala Ser Val Gln Trp Arg Gly Leu Asp

Thr Ser Leu Gly Ala Val Gln Ser Asp Thr Gly Arg Ser Val Leu Thr 65 70 75 80

Val Arg Asn Ala Ser Leu Ser Ala Ala Gly Thr Arg Val Cys Val Gly
85 90 95

Ser Cys Gly Gly Arg Thr Phe Gln His Thr Val Gln Leu Leu Val Tyr

Ala Phe Pro Asp Gln Leu Thr Val Ser Pro Ala Ala Leu Val Pro Gly

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| Asp | Pro 130 | Glu | Val | Ala | Cys | Thr 135 | Ala | His | Lys | Val | Thr 140 | Pro | Val | Asp | Pro |
|------------|------------|------------|------------|------------|-------------------|------------|------------|------------|------------|------------|------------|------------|--------------------|------------|------------|
| Asn 145 | Ala | Leu | Ser | Phe | Ser 150 | Leu | Leu | Val | Gly | Gly 155 | Gln | Glu | Leu | Glu | Gly 160 |
| Ala | Gln | Ala | Leu | Gly 165 | Pro | Glu | Val | Gln | Glu 170 | Glu | Glu | Glu | Glu | Pro 175 | Gln |
| Gly | Asp | Glu | Asp 180 | Val | Leu | Phe | Arg | Val 185 | Thr | Glu | Arg | Trp | Ar g 190 | Leu | Pro |
| Pro | Leu | Gly 195 | Thr | Pro | Val | Pro | Pro 200 | Ala | Leu | Tyr | CAa | Gln 205 | Ala | Thr | Met |
| Arg | Leu 210 | Pro | Gly | Leu | Glu | Leu 215 | Ser | His | Arg | Gln | Ala 220 | Ile | Pro | Val | Leu |
| His 225 | Ser | Pro | Thr | Ser | Pro 230 | Glu | Pro | Pro | Asp | Thr 235 | Thr | Ser | Pro | Glu | Ser 240 |
| Pro | Asp | Thr | Thr | Ser 245 | Pro | Glu | Ser | Pro | Asp 250 | Thr | Thr | Ser | Gln | Glu 255 | Pro |
| Pro | Asp | Thr | Thr 260 | Ser | Pro | Glu | Pro | Pro 265 | Asp | Lys | Thr | Ser | Pro 270 | Glu | Pro |
| Ala | Pro | Gln 275 | Gln | Gly | Ser | Thr | His 280 | Thr | Pro | Arg | Ser | Pro 285 | Gly | Ser | Thr |
| Arg | Thr 290 | Arg | Arg | Pro | Glu | Ile 295 | Ser | Gln | Ala | Gly | Pro 300 | Thr | Gln | Gly | Glu |
| Val 305 | Ile | Pro | Thr | Gly | Ser 310 | Ser | Lys | Pro | Ala | Gly 315 | Asp | Gln | Leu | Pro | Ala 320 |
| Ala | Leu | Trp | Thr | Ser 325 | Ser | Ala | Val | Leu | Gly 330 | Leu | Leu | Leu | Leu | Ala 335 | Leu |
| Pro | Thr | Tyr | His 340 | Leu | Trp | Lys | Arg | Cys 345 | Arg | His | Leu | Ala | Glu 350 | Asp | Asp |
| Thr | His | Pro 355 | Pro | Ala | Ser | Leu | Arg 360 | Leu | Leu | Pro | Gln | Val 365 | Ser | Ala | Trp |
| Ala | Gly 370 | Leu | Arg | Gly | Thr | Gly 375 | Gln | Val | Gly | Ile | Ser 380 | Pro | Ser | | |

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1721 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA



(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 4..1038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

| | (WI) DIGITION BESCHITTON. BEQ ID NO.5: | | | | | | | | | | | | | | | |
|-------------------|--|-------------------|----------------------|----------------------|-------------------|-------------------|-------------------|-------------------|----------------------|----------------------|-------------------|-------------------|-------------------|-------------------|----------------------|-----|
| AGO | Me | G GA t As 1 | T CG | G GG g Gl | C CTO y Leu | ı Ala | C CTC | C CTO | G CTO | G GCC 1 Ala 10 | a Gly | G CT | r cro | G GG 1 Gl | G CTC y Leu 15 | 48 |
| CTC Leu | Gl: | cc n Pr | G GGG | C TGC y Cys 20 | 3 Gly | CAC Glr | TCC Ser | CTC | C CAC 1 Glr 25 | ı Val | AAC Lys | G CCC | C CTC | G CAG | G GTG n Val | 96 |
| GAG Glu | Pro | C CC | G GAC O Glu 35 | ı Pro | GTG Val | GTG Val | GCC Ala | GTG Val 40 | . Ala | CTG Leu | GGC Gly | C GCC Ala | TCT Ser 45 | Arc | C CAG g Gln | 144 |
| CTC Leu | ACC Thr | C TG(Cys | Arc | CTG Leu | GAC Asp | TGC Cys | GCG Ala 55 | GAC Asp | CGC Arg | GGG Gly | GCC Ala | ACG Thr | Val | CAC Glr | TGG Trp | 192 |
| CGG Arg | GGC Gly 65 | rec | GAC Asp | ACC Thr | AGC Ser | CTG Leu 70 | GGC Gly | GCG Ala | GTG Val | CAG Gln | TCG Ser 75 | Asp | GCG Ala | GGC Gly | CGC Arg | 240 |
| AGC Ser 80 | GTC Val | CTC | ACC Thr | GTG Val | CGC Arg 85 | AAC Asn | GCC Ala | TCG Ser | CTG Leu | TCG Ser 90 | GCG Ala | GCC Ala | GGG Gly | ACC Thr | CGT Arg 95 | 288 |
| GTG Val | TGC Cys | GTG Val | GGC Gly | TCC Ser 100 | TGC Cys | GGG Gly | GGC Gly | CGC Arg | ACC Thr 105 | TTC Phe | CAG Gln | CAC His | ACC Thr | GTG Val 110 | CGG Arg | 336 |
| CTC Leu | CTT Leu | GTG Val | TAC Tyr 115 | GCC Ala | TTC Phe | CCG Pro | GAC Asp | CAG Gln 120 | CTG Leu | ACC Thr | ATC Ile | TCC Ser | CCG Pro 125 | GCA Ala | GCC Ala | 384 |
| CTG Leu | GTG Val | CCT Pro 130 | GGT Gly | GAC Asp | CCG Pro | GAG Glu | GTG Val 135 | GCC Ala | TGT Cys | ACG Thr | GCC Ala | CAC His 140 | AAA Lys | GTC Val | ACG Thr | 432 |
| CCT Pro | GTG Val 145 | GAC Asp | CCC Pro | AAT Asn | GCG Ala | CTC Leu 150 | TCC Ser | TTC Phe | TCC Ser | CTG Leu | CTC Leu 155 | CTG Leu | GGG Gly | GAC Asp | CAG Gln | 480 |
| GAA Glu 160 | CTG Leu | GAG Glu | GGG Gly | GCC Ala | CAG Gln 165 | GCT Ala | CTG Leu | GGC Gly | CCG Pro | GAG Glu 170 | GTG Val | GAG Glu | GAG Glu | GAG Glu | GAG Glu 175 | 528 |
| GAG Glu | GAG Glu | CCC Pro | CAG Gln | GAG Glu 180 | GAG Glu | GAG Glu | GAC Asp | GTG Val | CTG Leu 185 | TTC Phe | AGG Arg | GTG Val | Thr | GAG Glu 190 | CGC Arg | 576 |
| TGG (| CGG Arg | CTG Leu | CCG Pro 195 | ACC Thr | CTG Leu | GCA . Ala ' | Thr | CCT Pro 200 | GTC Val | CTG Leu | CCC Pro | Ala | CTC Leu 205 | TAC Tyr | TGC Cys | 624 |

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| CAG GCC ACG ATG AGG CTG CCT GGC TTG GAG CTC AGC CAC CGC CAG GCC Gln Ala Thr Met Arg Leu Pro Gly Leu Glu Leu Ser His Arg Gln Ala 210 215 220 | 672 |
|---|-------|
| ATC CCG GTC CTG CAC GGC CCG ACC TCC CGG GAG CCC CCC GAC ACG ACC Ile Pro Val Leu His Gly Pro Thr Ser Arg Glu Pro Pro Asp Thr Thr 225 230 235 | 720 |
| TCC CCG GAA CCC CGG GCC GCG ACC TCC CCG GAG ACC ACC CCC CAG CAG Ser Pro Glu Pro Arg Ala Ala Thr Ser Pro Glu Thr Thr Pro Gln Gln 240 255 | 768 |
| GGC TCC ACA CAC AGC CCC AGG AGC CCG GGC TCT ACC AGG ACT TGC CGC Gly Ser Thr His Ser Pro Arg Ser Pro Gly Ser Thr Arg Thr Cys Arg 260 265 270 | 816 |
| CCT GAG ATC TCC CAG GCT GGG CCC ACG CAG GGA GAA GTG ATC CCA ACA Pro Glu Ile Ser Gln Ala Gly Pro Thr Gln Gly Glu Val Ile Pro Thr 275 280 285 | 864 |
| GGC TCG TCC AAA CCT ACG GGT GAC CAG CTG CCC GCG GCT CTG TGG ACC Gly Ser Lys Pro Thr Gly Asp Gln Leu Pro Ala Ala Leu Trp Thr 290 295 300 | 912 |
| AGC AGT GCG GTG CTG GGA CTG CTG CTC CTG GCT TTG CCC ACC TAC CAC Ser Ser Ala Val Leu Gly Leu Leu Leu Ala Leu Pro Thr Tyr His 305 | 960 |
| CTC TGG AAA CGT TGC CGG CAC CTG GCT GAG GAC GGC GCC CAC CCA CCA Leu Trp Lys Arg Cys Arg His Leu Ala Glu Asp Gly Ala His Pro Pro 320 335 | 1008 |
| GCT TCT CTG AGT AGC CAG CCC TTC CCC CTG TGAAGGGAAA ATAGGTTGGA Ala Ser Leu Ser Ser Gln Pro Phe Pro Leu 340 345 | 1058 |
| CCCCTTCAAG CTGAGAACTG GTCGGGGCAA ACCTGCCTCC CATTCTATTC AAAGTCATCG | 1118 |
| CTCTGGTCAC AGAGAGGGAC GCACATTCTG ATTGCCTCCT TTGGAAAGGC TCATCAGAAA | 1178 |
| CTCAAAAGAA GGTGATCGTT TGTCCCGCCT ACCCGTGACC TGGAAGCCCC CGCCCCGCTC | 1238 |
| GAGTGACCCC TGACTTTCTG GACGGAACCA ACGTACTTCT TACATATATT GATTCATGTG | 1298 |
| TCATATCTCC CTAAAATGCG TAAAACCAGC TGTGCCCCGA CCACCTTGGG CCCCTGCCAT | 1358 |
| CAGGACCTCC TGAGGCTTTG GCAAATAAAC CTCCTAAAAG GATAGAAACT GAAACTTGTG | 1418 |
| GCCGGGCGCG GTGGCTCAAG CCTGTAATCC CAGCACTTTG GGAGGCCGAG GTGGGTGGAT | · · • |
| CACGAGGTCA GGAGATCGAG ACCATCCTGG CTAACCCCGTG AAACCCCGTC TCTACTAAAA | |
| AAATACAAAA ATTAGCCGGG AGCGGTGGCG GGCGCCTGTA GTCCCAGCTA CTCGGGAGGC | |
| TGAGGCAGGA GAATGGCGTG AACCCGGGAG GCGGAGCTTG CAGTGAGCTG AGATCCGGCC | |
| ACTGCACTCC AGCCTGGGGG ACAGAGCGAG ACTCCGTCTC AAAAAAAAAA | |
| AAA | 1721 |

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(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 345 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Asp Arg Gly Leu Ala Leu Leu Ala Gly Leu Leu Gly Leu Leu 1 5 10 15

Gln Pro Gly Cys Gly Gln Ser Leu Gln Val Lys Pro Leu Gln Val Glu 20 25 30

Pro Pro Glu Pro Val Val Ala Val Ala Leu Gly Ala Ser Arg Gln Leu 35 40 45

Thr Cys Arg Leu Asp Cys Ala Asp Arg Gly Ala Thr Val Gln Trp Arg
50 55 60

Gly Leu Asp Thr Ser Leu Gly Ala Val Gln Ser Asp Ala Gly Arg Ser 65 70 75 80

Val Leu Thr Val Arg Asn Ala Ser Leu Ser Ala Ala Gly Thr Arg Val 85 90 95

Cys Val Gly Ser Cys Gly Gly Arg Thr Phe Gln His Thr Val Arg Leu 100 105 110

Leu Val Tyr Ala Phe Pro Asp Gln Leu Thr Ile Ser Pro Ala Ala Leu 115 120 125

Val Pro Gly Asp Pro Glu Val Ala Cys Thr Ala His Lys Val Thr Pro 130 135

Val Asp Pro Asn Ala Leu Ser Phe Ser Leu Leu Leu Gly Asp Gln Glu 145 150 155 160

Leu Glu Gly Ala Gln Ala Leu Gly Pro Glu Val Glu Glu Glu Glu Glu 165 170 175

Glu Pro Gln Glu Glu Asp Val Leu Phe Arg Val Thr Glu Arg Trp 180 185 190

Arg Leu Pro Thr Leu Ala Thr Pro Val Leu Pro Ala Leu Tyr Cys Gln
195 200 205

Ala Thr Met Arg Leu Pro Gly Leu Glu Leu Ser His Arg Gln Ala Ile 210 215 220

Pro Val Leu His Gly Pro Thr Ser Arg Glu Pro Pro Asp Thr Thr Ser 225 230 235 240

Pro Glu Pro Arg Ala Ala Thr Ser Pro Glu Thr Thr Pro Gln Gln Gly 245 250 255

335

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| Ser | Thr | His | Ser 260 | Pro | Arg | Ser | Pro | Gly 265 | Ser | Thr | Arg | Thr | Cys 270 | Arg | Pro |
|------------|------------|------------|------------|-----|------------|------------|------------|------------|-----|------------|------------|------------|------------|-----|------------|
| Glu | Ile | Ser 275 | Gln | Ala | Gly | Pro | Thr 280 | Gln | Gly | Glu | Val | Ile 285 | Pro | Thr | Gly |
| Ser | Ser 290 | Lys | Pro | Thr | Gly | Asp 295 | Gln | Leu | Pro | Ala | Ala 300 | Leu | Trp | Thr | Ser |
| Ser 305 | Ala | Val | Leu | Gly | Leu 310 | Leu | Leu | Leu | Ala | Leu 315 | Pro | Thr | Tyr | His | Leu 320 |
| Trp | Lys | Arg | Сув | Arg | His | Leu | Ala | Glu | Asp | Gly | Ala | His | Pro | Pro | Ala |

Ser Leu Ser Ser Gln Pro Phe Pro Leu 340

- (2) INFORMATION FOR SEQ ID NO:7:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid

 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTCTACTGCC AGGCCACG

18

- (2) INFORMATION FOR SEQ ID NO:8:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single (D) TOPOLOGY: unknown
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AGCCTGGGAG ATCTCAGGG

19

- (2) INFORMATION FOR SEQ ID NO:9:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

 - (B) TYPE: nucleic acid (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9: GCCACGATGA GGCTGCCTGG

20

(2) INFORMATION FOR SEQ ID NO:10:

GGACTAGTGG TTTGGACGAG CCTGTTG

27

| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: unknown | |
|--|----|
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10: | |
| GTGGAGCCTG GGCTCCTGGG | 20 |
| (2) INFORMATION FOR SEQ ID NO:11: | |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 32 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11: | |
| GGAAGCTTCC ACCATGGATT TCGGACTGGC CC | 32 |
| (2) INFORMATION FOR SEQ ID NO:12: | |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 26 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12: | |
| CCGACTAGTG TCGGGCTGTG CAGGAC | 26 |
| (2) INFORMATION FOR SEQ ID NO:13: | |
| (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear | |
| (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13: | |